FIGURE 1

MFRLRSWASSTTGSRYGSAFCGSPTLAWCVCVPVCYGESRILRVKVVSG

IDLAKKDIFGASDPYVKLSLYVADENRELALVQTKTIKKTLNPKWNEEF
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^

YFRVNPSNHRLLFEVFDENRLTRDDFLGQVDVPLSHLPTEDPTMERPYT
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^

FKDFLLRPRSHKSRVKGFLRLKMAYMPKNGGQDEENSDQRDDMEHGWEV

VDSNDSASQHQEELPPPPLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPS
* *

LMDVSSESDNNIRQINQEAAHRRFRSRRHISEDLEPEPSEGGDVPEPWE
*

TISEEVNIAGDSLGVVLPPPPASPGSRTSPQELSEELSRRLQITPDSNG

EQFSSLIQREPSSRLRSCSVTDAVAEQGHLPPPSVAYVHTTPGLPSGWE
* * * * * * * *

ERKDAKGRTYYVNHNNRTTTWTRPIMQLAEDGASGSATNSNNHLIEPQI
* *

RRPRSLSSPTVTLXAPLEGAKDSPVRRAVKDTLSNPQSPQPSPYNSPKP

QHKVTQSFLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFPVHMRSK

TSLNPNDLGPLPPGWEERIHLDGRTFYIDHNSKITQWEDPRLQNPAITG
* *

PAVPYSREFKQKYDYFRKKLKKPADIPNRFEMKLHRNNIFEESYRRIMS

VKRPDVLKARLWIEFESEKGLDYGGVAREWFFLLSKEMFNPYYGLFEYS

ATDNYTLQINPNSGLCNEDHLSYFTFIGRVAGLAVFHGKLLDGFFIRPF

YKMMLGKQITLNDMESVDSEYYNSLKWILENDPTELDLMFCIDEENFGQ

TYQVDLKPNGSEIMVTNENKREYIDLVIQWRFVNRVQKQMNAFLEGFTE

LLPIDLIKIFDENELELLMCGLGDVDVNDWRQHSI<u>YKNGYCPNHPVIQW</u>

<u>FWKAVLLMDAEKRIRLLQFVTGTSRVPMNGFAELYGSNGPQLFTIEQWG</u>

<u>SPEKLPRAHTCFNRLDLPPYETFEDLREKLLMAVENAQGFEGVD</u>.

FIGURE 2

```
  1  S R F S S S S S T V A C P G R G R A R P V C W K R S E M A . . T C A V E V F G L   P46934
  1  - M F R L R S W A S S T T G S R Y G S A F C - G S P T L A W C V C V P V C Y G -   ZGGBP-1

 39  L E D E E N S R I V R V R V I A G I G L A K K D I L G A S D F Y V R V T L Y D P   P46934
 38  . . . . E S R I L R V K V V S G I D L A K K D I F G A S D P Y V K L S L Y V A   ZGGBP-1

 79  M N G V . L T S V Q T K T I K K S L N P K W N E E I L F R V H P Q Q H R L L F E   P46934
 73  D E N R E L A L V Q T K T I K K T L N P K W N E E P Y F R V N P S N H R L L F E   ZGGBP-1

118  V F D E N R L T R D D F L G Q V D V P L Y P L P T E N P R L E R P Y T F K D P V   P46934
113  V F D E N R L T R D D F L G Q V D V P L S H L P T E D P T M E R P Y T F K D F L   ZGGBP-1

158  L H P R S H K S R V K G Y L R L K M T Y L P K T S G S E D D N A E Q A E E L E P   P46934
153  L R P R S H K S R V K G F L R L K M A Y H P K N G G Q D E E N S D R D D M E H   ZGGBP-1

198  G W V V L D Q P D A A C H L Q Q Q Q E P S P L P P G W E E R Q D I L G R T Y Y V   P46934
193  G W E V V D S N D S A S Q H Q E E L P P P P L P P G W E E K V D N L G R T Y Y V   ZGGBP-1

238  N H E S R R T Q W K R P T P Q D N L T D A E N G N I Q L Q . . . A Q R A F T T R   P46934
233  N H N N R T T Q W H R P S L M D V S S E S D N N I R Q I N Q E A A H R R F R S R   ZGGBP-1

275  R Q I S E . . F T E S V D N Q E S S E N W E I I R E D E A T M Y S S Q A F P S P   P46934
273  R H I S E D L E P E P S E G G D V P F P W E T I S E E V N I A G D S L G V V L P   ZGGBP-1

313  P P S N L D V . . . P T H L A E E L N A R L T I F G N S A V S Q P A S S S N H   P46934
313  P P P A S P G S R T S P Q E L S E E L S R R L Q I T P D S N G E Q F S S L I Q R   ZGGBP-1

350  S S R . . . R G S L Q A Y T F E E Q P T L P . . . . . V L L P T S G L P P G W E   P46934
353  E P S S R L R S C S V T D A V A E Q G H L P P P S V A Y V H T T P C L P S G W E   ZGGBP-1

383  E K Q D E R G R S Y Y V D M N S R T T T W T K P T V Q . . . . . . . . A T V E   P46934
393  E R K D A K G R T Y Y V N H N N R T T T W T R P I M Q L A E D G A S G S A T N S   ZGGBP-1

414  T S Q L T S S Q S S . . . . . . . . . . . . A G P Q S Q A S T S D . . . . .   P46934
433  N N H L I E P Q I R R P R S L S S P T V T L X A P L E G A K D S P V R R A V K D   ZGGBP-1

435  . . S G Q Q V T Q P S L . . . . . . . . . E I E Q G F L P K G W E V R H A P N G R   P46934
473  T L S N P Q S P Q P S P Y N S P K P Q H K V T Q S F L P P G W E M R I A P N G R   ZGGBP-1

464  P F F I D H N T K T T T W E D P R L K I P A H L R G K T S L D T S N D L G P L P   P46934
513  P F F I D H N T K T T T W E D P R L K F P V H M R S K T S L N - P N D L G P L P   ZGGBP-1

504  P G W E E R T H T D G R I F Y I N H N I K R T Q W E D P R L E N V A I T G P A V   P46934
552  P G W E E R I H L D G R T F Y I D H N S K I T Q W E D P R L Q N P A I T G P A V   ZGGBP-1

544  P Y S R D Y K R K Y E F F R R K L K K Q N D I P N K F E M F L R R A T V L E D S   P46934
592  P Y S R E F K Q K Y D Y F R K K L K K P A D I P N R P E M F L H R N N I F E E S   ZGGBP-1

584  Y R R I M G V K R A D F L K A R L W I E F D G E K G L D Y G G V A R E W F F L I   P46934
632  Y R R I M S V K R P D V L K A R L W I E P E S E K G L D Y G G V A R E W F F L L   ZGGBP-1

624  S K E M F N P Y Y G L P E Y S A T D N Y T L Q I N P N S G L C N E D H L S Y F K   P46934
672  S K E M F N P Y Y G L F E Y S A T D N Y T L Q I N P N S G L C N E D H L S Y F T   ZGGBP-1

664  F I G R V A G M A V Y H G K L L D G F F I R P F Y K M M L H K P I T L H D M E S   P46934
712  F I G R V A G L A V F H G K L L D G F F I R P F Y K M M L G K Q I T L N D M E S   ZGGBP-1

704  V D S E Y Y N S L P W I L E N D P T E L D L R F I I D E E L F G Q T H Q H E L K   P46934
752  V D S E Y Y N S L F W I L E N D P T E L D L M F C I D E E N F G Q T Y Q V D L K   ZGGBP-1

744  N G G S E I V V T N K N K X E Y I Y L V I Q W R F V N R I Q K Q M A A F K F G F   P46934
792  P N G S E I M V T N E N K R E Y I D L V I Q W R F V N R V Q K Q M N A F L E G F   ZGGBP-1

784  F E L I P Q D L I K I F D E N E L E L L M C G L G D V D V N D W R E H T K Y K N   P46934
832  T E L L P I D L I K I F D E N F L E L L M C G L G D V D V N D W R Q H S I Y K N   ZGGBP-1

824  G Y S A N H Q V I Q W F W K A V L M M D S E K R I R L L Q F V T G T S R V P M N   P46934
872  G Y C P N H P V I Q W F W K A V L L M D A E K R I R L L Q F V T G T S R V P M N   ZGGBP-1

864  G F A E L Y G S N G P Q S F T V E Q W G T P E K L P R A H T C F N R L D L P P Y   P46934
912  G F A E L Y G S N G P Q L F T I E Q W G S P E K L P R A H T C F N R L D L P P Y   ZGGBP-1

904  E S F E E L W D K L Q M A I E N T Q G F D G V . D   P46934
952  E T F E D L R E K L L M A V E N A Q G F E G V D   ZGGBP-1
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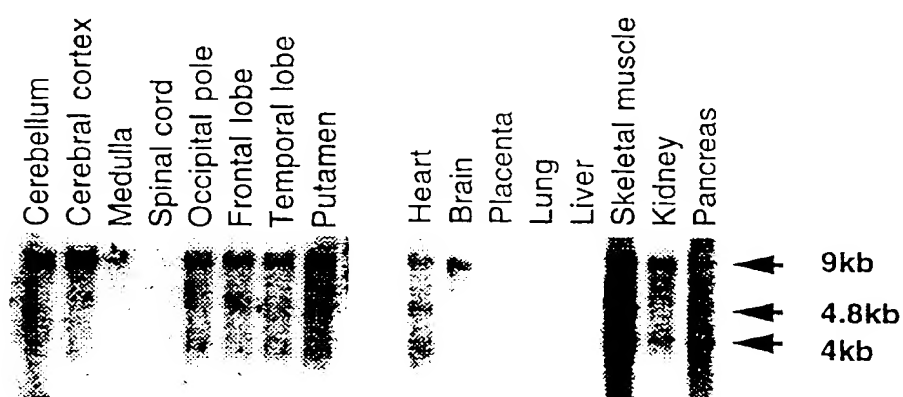
FIGURE 3

FIGURE 4

Mouse ZGGBP-1 / Human ZGGBP-1 nucleotide sequence alignment

FIGURE 5

```
1     CGG - - - - - - - TA- - -TCAGCAGAGG- - -                     Pub-3.seq
1     CAAGCCGCGCAATTAACCCTCACTAAAGGGAACACCAACAC                    ZGGBP1.seq

16    - - - - - - TGTGT- - -                  -ACGGGCACTG-           Pub-3.seq
41    GTCGCCAGGACTGCGCCGTTCGCTGCGCTCATAGGCGGCG                     ZGGBP1.seq

31    CTTT- - -AAAACTGGGAAGGA- - -GG- -                             Pub-3.seq
81    ATTTCATCAAGGGTGGCAAGGATCGCCTGGTCGACGGTCA                     ZGGBP1.seq

51    - - - - - - - - - - - - - - - - - - - - - - AA                 Pub-3.seq
121   GGTCGTCCTCGACGCGGGGTTGCCCTCCTCGTCGTTCCAG                     ZGGBP1.seq

53    GACGAG- - - -GCCAGGGAG- - -                                  Pub-3.seq
161   GGTGAGTGGGCGGATACCAGGTGTCCAACCGGGAAGGTACGG                   ZGGBP1.seq

68    - - - - - - - - - - -CCGGAG- - -                              Pub-3.seq
201   CCCGACACCTCGACAATCGGCGCATCGTCGAAGTGCTTGG                     ZGGBP1.seq

74    - - - - - -GGTCA- - -CCAAGGTA- - -GAT                          Pub-3.seq
241   AAAAGCGCTCCAGGTCGATGGTGGCCGAGGTGATGATGAC                     ZGGBP1.seq

90    TTCCAG- - -CAGCGC- - -                      -TAG             Pub-3.seq
281   TTTCAGGTCGGGGCGAICGCGGCCAACAGGGTCTTGAGGTAG                   ZGGBP1.seq

105   TCCAGCTGAA- -CACTTTCCAG- - -                  -CCT           Pub-3.seq
321   CCGAGCAGGAGTCGATGTTCAGGCTGCGTTCGTTGGGCTT                     ZGGBP1.seq

128   TGTT- - - - - - - - - - - - - - -TTTCAGCAG- - -                Pub-3.seq
361   CGTCGACGACAGGCCTCGCGTTATGGCTCCGCTTTCTGCGG                    ZGGBP1.seq

141   CTTT- - - - - - - - - - - - - - -                             Pub-3.seq
401   CTCTCCTACCCTGGCATGGTGTGTGTCCCTGTGTGC                         ZGGBP1.seq

145   - - - - - -GAGGAAAAGT- - -A T- -                              Pub-3.seq
441   TACGGAGAGTCCGTATTCTCAGAGTAAAAGTTGTYTCTG                      ZGGBP1.seq
```

FIGURE 5 continued

```
157  -----------------AGTGA  Pub-3.seq
481  GAATWGATCTCGCCAAAAAGGACATCTTTGGAGCCAGTGA  ZGGBP1.seq

162  TCCGTATGTGAAACTTTCATTGTACGTAGCGGATGAGAAT  Pub-3.seq
521  TCCGTATGTGAAACTTTCATTGTACGTAGCGGATGAGAAT  ZGGBP1.seq

202  AGAGAACTTGCTTTGGTTCCAGACAAAAAACAATTAAAAAGA  Pub-3.seq
561  AGAGAACTTGCTTTGGTTCCAGACAAAAAACAATTAAAAAGA  ZGGBP1.seq

242  CACTGAACCCAAAAATGGAATGAAGAATTTTATTTCAGGGT  Pub-3.seq
601  CACTGAACCCAAAAATGGAATGAAGAATTTTATTTCAGGGT  ZGGBP1.seq

282  AAACCCATCTAATCACAGACTCCTATTTGAAGTATTTGAC  Pub-3.seq
641  AAACCCATCTAATCACAGACTCCTATTTGAAGTATTTGAC  ZGGBP1.seq

322  GAAATAGACTGACACGAGACGGCTTCCTGGGCCAGGTGG  Pub-3.seq
681  GAAATAGACTGACACGAGACGACTTCCTGGGCCAGGTGG  ZGGBP1.seq

362  ACGTGCCCCTTAGTCACCTTCCGACAGAAGATCCAACCAT  Pub-3.seq
721  ACGTGCCCCTTAGTCACCTTCCGACAGAAGATCCAACCAT  ZGGBP1.seq

402  GGAGCGACCCTATACATTTAAGGACTTTCCTCTCAGACCA  Pub-3.seq
761  GGAGCGACCCTATACATTTAAGGACTTTCCTCTCAGACCA  ZGGBP1.seq

442  AGAAGTCATAAGTCTCGAGTTAAGGGATTTTTGCGATTGA  Pub-3.seq
801  AGAAGTCATAAGTCTCGAGTTAAGGGATTTTTGCGATTGA  ZGGBP1.seq

482  AAATGGCCTATATGCCAAAAAAATGGAGGTCAAGATGAAGA  Pub-3.seq
841  AAATGGCCTATATGCCAAAAAAATGGAGGTCAAGATGAAGA  ZGGBP1.seq

522  AAACAGTGACCAGAGGGATGACATGGAGCATGGGGAA  Pub-3.seq
881  AAACAGTGACCAGAGGGATGACATGGAGCATGGGGAA  ZGGBP1.seq

562  GTTGTTGACTCAAATGACTCGGCTTCTCAGCACCAAGAGG  Pub-3.seq
921  GTTGTTGACTCAAATGACTCGGCTTCTCAGCACCAAGAGG  ZGGBP1.seq
```

FIGURE 5 continued

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602  AACTTCCTCCTCTGCCTCCCGGGTGGGGAAGAAAA  Pub-3.seq
961  AACTTCCTCCTCTGCCTCCCGGGTGGGGAAGAAAA  ZGGBP1.seq

642  AGTGGACAAATTTAGGCCGAACTTACTTGTCAACCACAAC  Pub-3.seq
1001 AGTGGACAAATTTAGGCCGAACTTACTTGTCAACCACAAC  ZGGBP1.seq

682  AACCGGACCACTCAGTGGCACAGACCAAGCCTGATGGACG  Pub-3.seq
1041 AACCGGACCACTCAGTGGCACAGACCAAGCCTGATGGACG  ZGGBP1.seq

722  TGTCCTCGGAGTCGGACAATAACATCAGAGATCAACCA  Pub-3.seq
1081 TGTCCTCGGAGTCGGACAATAACATCAGAGATCAACCA  ZGGBP1.seq

762  GGAGGCAGCACACCGGCGCTTCCCGCAGGCACATC  Pub-3.seq
1121 GGAGGCAGCACACCGGCGCTTCCCGCAGGCACATC  ZGGBP1.seq

802  AGCGAAGACTTGGAGCCCGGCCCTCGGGAGGGGATG  Pub-3.seq
1161 AGCGAAGACTTGGAGCCCGGCCCTCGGGAGGGGATG  ZGGBP1.seq

842  TCCCCGAGCCTTGGGAGACCATTTCAGAGGAAGTGAATAT  Pub-3.seq
1201 TCCCCGAGCCTTGGGAGACCATTTCAGAGGAAGTGAATAT  ZGGBP1.seq

882  CGCTGGACTCTCTCGGTCTCTGCCCCCCACCG  Pub-3.seq
1241 CGCTGGAGACTCTCTCGGTGGTTTGCCCCCCACCG  ZGGBP1.seq

922  GTCTCCCCAGGATCTCGGAGCCCTCGGAGCTGTCAG  Pub-3.seq
1281 GCTCCCCAGGATCTCGGAGCCCTCGGAGCTGTCAG  ZGGBP1.seq

962  AGGAACTAAGCAGAAGGCTTCAGAGATCACTCCAA  Pub-3.seq
1321 AGGAACTAAGCAGAAGGCTTCAGAGATCACTCCAA  ZGGBP1.seq

1002 TGGGAACAGTTCAGCTCTTTGATTCAAAGAGAACCCTCC  Pub-3.seq
1361 TGGGAACAGTTCAGCTCTTTGATTCAAAGAGAACCCTCC  ZGGBP1.seq

1042 TCAAGGTTGAGGTCATGCAGTGTCACCGACGCAGTTGCAG  Pub-3.seq
1401 TCAAGGTTGAGGTCATGCAGTGTCACCGACGCAGTTGCAG  ZGGBP1.seq

1082 AACAGGGCCATCTACCACCGGCCTATGTACA  Pub-3.seq
1441 AACAGGGCCATCTACCACCGGCCTATGTACA  ZGGBP1.seq
```

FIGURE 5 continued


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                                              Pub-3.seq
                                              ZGGBP1.seq

1122 TACCACGCCGGGTCTGCCTTCAGGCTGGGAAGAAAA      Pub-3.seq
1481 TACCACGCCGGGTCTGCCTTCAGGCTGGGAAGAAAA      ZGGBP1.seq

1162 GATGCTAAGGGGCGCACATACTATGTCAATCATAACAATC  Pub-3.seq
1521 GATGCTAAGGGGCGCACATACTATGTCAATCATAACAATC  ZGGBP1.seq

1202 GAACCACAACTTGGACTCGATCATGCAGCTTGCAGA      Pub-3.seq
1561 GAACCACAACTTGGACTCGATCATGCAGCTTGCAGA      ZGGBP1.seq

1242 AGATGGTGCCGTCCGGGATCAGCCACAAACAGTAACAACCAT Pub-3.seq
1601 AGATGGTGCCGTCCGGGATCAGCCACAAACAGTAACAACCAT ZGGBP1.seq

1282 CTAATCGAGCCTCAGATCCGGCCGCCCCGGTAGCCTCAGCT Pub-3.seq
1641 CTAATCGAGCCTCAGATCCGGCCGCCCCGGTAGCCTCAGCT ZGGBP1.seq

1322 CGCCAACAGTAACTTTATCTGCCCCCGCCTGGAGGGTGCCAA Pub-3.seq
1681 CGCCAACAGTAACTTTATYTGCCCCCGCCTGGAGGGTGCCAA ZGGBP1.seq

1362 GGACTCACCCCGTACGTCGGGGCTGTGAAAGACACCCCTTTCC Pub-3.seq
1721 GGACTCACCCCGTACGTCGGGGCTGTGAAAGACACCCCTTTCC ZGGBP1.seq

1402 AACCCACACAGTCCCCCAGCCATCACCTTACAACTCCCCCA Pub-3.seq
1761 AACCCACACAGTCCCCCAGCCATCACCTTACAACTCCCCCA ZGGBP1.seq

1442 AACCACACACAAAGTCACACAGAGCTTCTTGCCACCCGG   Pub-3.seq
1801 AACCACACACAAAGTCACACAGAGCTTCTTGCCACCCGG   ZGGBP1.seq

1482 CTGGGAAATGAGGATAGCCGGCCAAACGGCCCGGCCCTTCTTC Pub-3.seq
1841 CTGGGAAATGAGGATAGCCGGCCAAACGGCCCGGCCCTTCTTC ZGGBP1.seq

1522 ATTGATCATAACAAAAGACACAACCTGGGAAGATCCAC    Pub-3.seq
1881 ATTGATCATAACAACACTACAACCTACCA             ZGGBP1.seq
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FIGURE 5 continued

PCT/GB98/02259

09/463844

FIGURE 5 continued

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2082  TAATGAGGATCATTTGTCCTACTTCACTTTTATTGGAAGA   Pub-3.seq
2441  TAATGAGGATCATTTGTCCTACTTCACTTTTATTGGAAGA   ZGGBP1.seq

2122  GTTGCTGGTCTGGCCGTATTTCATGGGAAGCTCTTAGATG   Pub-3.seq
2481  GTTGCTGGTCTGGCCGTATTTCATGGGAAGCTCTTAGATG   ZGGBP1.seq

2162  GTTTCTTCATTAGACCATTTTACAAGATGATGTTGGGAAA   Pub-3.seq
2521  GTTTCTTCATTAGACCATTTTACAAGATGATGTTGGGAAA   ZGGBP1.seq

2202  GCAGATAACCCTGAATGACATGGAATCTGTGGATAGTGAA   Pub-3.seq
2561  GCAGATAACCCTGAATGACATGGAATCTGTGGATAGTGAA   ZGGBP1.seq

2242  TATTACAACTCTTTGAAATGGATCCTGGAGAATGACCCTA   Pub-3.seq
2601  TATTACAACTCTTTGAAATGGATCCTGGAGAATGACCCTA   ZGGBP1.seq

2282  CTGAGCTGGACCTCATGTTCTGCATAGACGAAGAAAACTT   Pub-3.seq
2641  CTGAGCTGGACCTCATGTTCTGCATAGACGAAGAAAACTT   ZGGBP1.seq

2322  TGGACAGACATATCAAGTGGATTTGAAGCCCAATGGGTCA   Pub-3.seq
2681  TGGACAGACATATCAAGTGGATTTGAAGCCCAATGGGTCA   ZGGBP1.seq

2362  GAAATAATGGTCACAAATGAAAAACAAAAGGGAATATCG   Pub-3.seq
2721  GAAATAATGGTCACAAATGAAAAACAAAAGGGAATATCG   ZGGBP1.seq

2402  ACTTAGTCATCCAGTGGAGATTTGTGAACAGGGTCCAGAA   Pub-3.seq
2761  ACTTAGTCATCCAGTGGAGATTTGTGAACAGGGTCCAGAA   ZGGBP1.seq

2442  GCAGATGAACGCCTTCTTGGAGGGATTCACAGAACTACTT   Pub-3.seq
2801  GCAGATGAACGCCTTCTTGGAGGGATTCACAGAACTACTT   ZGGBP1.seq

2482  CCTATTTGATTAAAATTTTTGATGAAAATGAGCTGG   Pub-3.seq
2841  CCTATTTGATTAAAATTTTTGATGAAAATGAGCTGG   ZGGBP1.seq
```

FIGURE 5 continued

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2522  AGTTGCTCATGTGCGGCCTCGGTGATGTGGATGTGAATGA  Pub-3.seq
2881  AGTTGCTCATGTGCGGCCTCGGTGATGTGGATGTGAATGA  ZGGBP1.seq

2562  CTGGAGACAGCATTCTATTTACAAGAACGGCTACTGCCCA  Pub-3.seq
2921  CTGGAGACAGCATTCTATTTACAAGAACGGCTACTGCCCA  ZGGBP1.seq

2602  AACCACCCCGTCATTCAGTGGTTCTGGAAGGCTGTGCTAC  Pub-3.seq
2961  AACCACCCCGTCATTCAGTGGTTCTGGAAGGCTGTGCTAC  ZGGBP1.seq

2642  TCATGGACGCCGAAAAGCCGTATCCGGTTACTGCAGTTTGT  Pub-3.seq
3001  TCATGGACGCCGAAAAGCCGTATCCGGTTACTGCAGTTTGT  ZGGBP1.seq

2682  CACAGGGACATCGCGAGTACCTATGGATTTGCCGAA  Pub-3.seq
3041  CACAGGGACATCGCGAGTACCTATGGATTTGCCGAA  ZGGBP1.seq

2722  CTTTATGGTTCCAATGGTCCTCAGCTGTTTACAATAGAGC  Pub-3.seq
3081  CTTTATGGTTCCAATGGTCCTCAGCTGTTTACAATAGAGC  ZGGBP1.seq

2762  AATGGGGCAGTCCTGAGAAACTCCCCAGAGCTCACACATG  Pub-3.seq
3121  AATGGGGCAGTCCTGAGAAACTGCCCAGAGCTCACACATG  ZGGBP1.seq

2802  CTTTAATCGGCCTTGACTTACCTCCATTCTCACCTTTGAA  Pub-3.seq
3161  CTTTAATCGGCCTTGACTTACCTCCATATGAAACCTTTGAA  ZGGBP1.seq

2842  GATTTACGAGAGAAACTTCTCATGGCCGTGGAAAATGCTC  Pub-3.seq
3201  GATTTACGAGAGAAACTTCTCATGGCCGTGGAAAATGCTC  ZGGBP1.seq

2882  AAGGATTTGAAGGGGTGGATTAAGCACCCTGCCTCGGG  Pub-3.seq
3241  AAGGATTTGAAGGGGTGGATTAAGCACCCTGTGCCTCGGG  ZGGBP1.seq

2922  GGTGGTTGTTCTTCAAGCAAGTTCTTGCACTTTTGCA  Pub-3.seq
3281  GGTGGTTGTTCTTCAAGCAAGTTCTTGCACTTTTGCA  ZGGBP1.seq

2962  TTTGCCTAACAGACTTTTTGCAGAGGCGATGGCAGAGCA  Pub-3.seq
3321  TTTGCCTAACAGACTTTTTGCAGAGGCGATGGCAGAGCA  ZGGBP1.seq

3002  GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA  Pub-3.seq
3361  GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA  ZGGBP1.seq
```

FIGURE 5 continued

3208 - AGACAAGTACTTTGAGAGAATTTCCAATATAATATTAGAC Pub-3.seq / ZGGBP1.seq

3208 - ATAATGATAATTTTTCCATACTCAGAATGAAAAACTGGA -AAAAAA Pub-3.seq / ZGGBP1.seq

3214 - TATTACGTTTTTGTTTGGGTTTTTTGTACAAATTTAG Pub-3.seq / ZGGBP1.seq

3214 - CTAATAGCTACAGGCTGAGAGAATTGTAACATAGCATGAC Pub-3.seq / ZGGBP1.seq

3214 - AAATTTGTTGTTGACTTGAAAGGAATCACACCATTATTCC Pub-3.seq / ZGGBP1.seq

3214 - TTAGAAGTAATTACATGTGTTCTAACACATTTGAGACAGG Pub-3.seq / ZGGBP1.seq

3214 - GTTGGACTCCCATTCTCATCCGAGAAATTACTTAACCCT Pub-3.seq / ZGGBP1.seq

3214 - TCCTGGGCGCTGTACAGTCATCTTTATTCTATTTCCTCT Pub-3.seq / ZGGBP1.seq

3214 - TTGCTGTTTGTTGTAGTAGAGACATTTTGAATGAAACTTGGCA Pub-3.seq / ZGGBP1.seq

3214 - CTGCTTGATTCAAAACTGTGGAAACCAGATCTGTTTAGTC Pub-3.seq / ZGGBP1.seq

3214 - TCCTGTTGTTTGTATGCGTTTGCTAATGGTAGCTAAATAACCA Pub-3.seq / ZGGBP1.seq

3214 - GTTTTGTTGTAAATGCACCAATTCTGAAGGCACTTTATG Pub-3.seq / ZGGBP1.seq

3214 - TACTACATGGAGGTCATATCTGGTTTTGTTTTTATTTTT Pub-3.seq / ZGGBP1.seq

3840
3880
3920
3960
4000
4040
4080
4120
4160
4200
4240
4280
4320

FIGURE 5 continued

```
3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4360  TATCATGAACATTAAATGTGATGATGATTTCTTTTCCCTG                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4400  CACACATCTTTCCGGTGCAATATCTATCAATTGTGAATCT                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4440  GGCTGCTGGTGTATAAAAACCTGGATGTAAAGCTGAGCCT                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4480  ACAGACCTGTCCTCACCAACTGTTTTGTGATTTCTACTCA                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4520  ACTACAAAGATTTATTTAATGTACTCTTAATCTAACTGAG                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4560  TTTGTTACCAATGACCTGTTGCATGCTTCAATACCGTGT                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4600  ACTGCCTGAGTTGTGCCTCTTGTGTGCTAGATTAAAAGTG                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4640  AGACAGAGACTTGACTTGATCCTCTGAGCCTCAAGCTATT                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4680  GAGCTGGTAGTGGCAGAGGACTGAGGGTACCTGCACAGTT                          ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4720  TGATTCTTTTCCCACGTTCTCCATTGCAGAATTG                                ZGGBP1.seq

3214 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -                      Pub-3.seq
4760  TCGTGCGTTTGAGAAAACACCTGAGGCAGTGTGGGAGTTG                          ZGGBP1.seq
```

FIGURE 5 continued

```
                                                                           Pub-3.seq
3214 - - - - - - - - - - - - - - - - - - - - - - - - AACGACCCTGCTGTCCTTTTAACCTGTGTTGTCCTAGAC
4800                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3214 - - - - - - - - - - - - - - - - - - - - - - - - CTGTCGGGGCAGTCAGGGGACACTAGAGATTTGATCTCAT
4840                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3214 - - - - - - - - - - - - - - - - - - - - - AAAAA A GCGAGTCATCAATAGGACAAAAAAGTTGTGGTTTGGGGAG
4880                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3220 - - - - - - - - - - - - - - - - - - - - - - - - GTCTGTTTGTTACATAAAAAAGGACACCTTTCGGTAAGAAA
4920                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3220 - - - - - - - - - - - - - - - - - - - - - - - - TTGCCGTTTTACCCTGCCCCTGGCATGTGAGAAGCC
4960                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3220 - - - - - - - - - - - - - - - - - - - - - - - - ATGGAAGGTTGTGTGGTTGTAAATGAGTTGTCTAAAGGGGTG
5000                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3220 - - - - - - - - - - - - - - - - - - - - AAAAA AA CAGAGGCCTGAGGTTTCTAAAAGAAGGTAGATTTCTACAG
5040                                                                        ZGGBP1.seq

                                                                           Pub-3.seq
3226 AGCTGAGTGTTGGTTCCTTTTTCTTATTGGTTGAAAATTA                              ZGGBP1.seq
5080

                                                                           Pub-3.seq
3226 CCTGGTAGTGATCAGAAAAACTTAGATGCTATGTAACTC                               ZGGBP1.seq
5120
```

Decoration 'Decoration #1': Box residues that match the Consensus exactly.
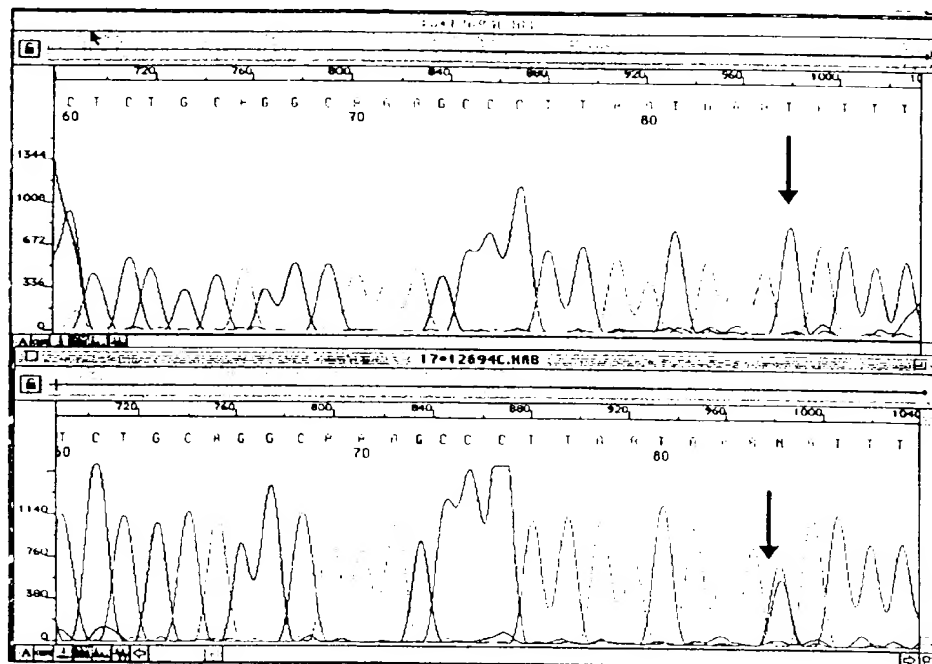
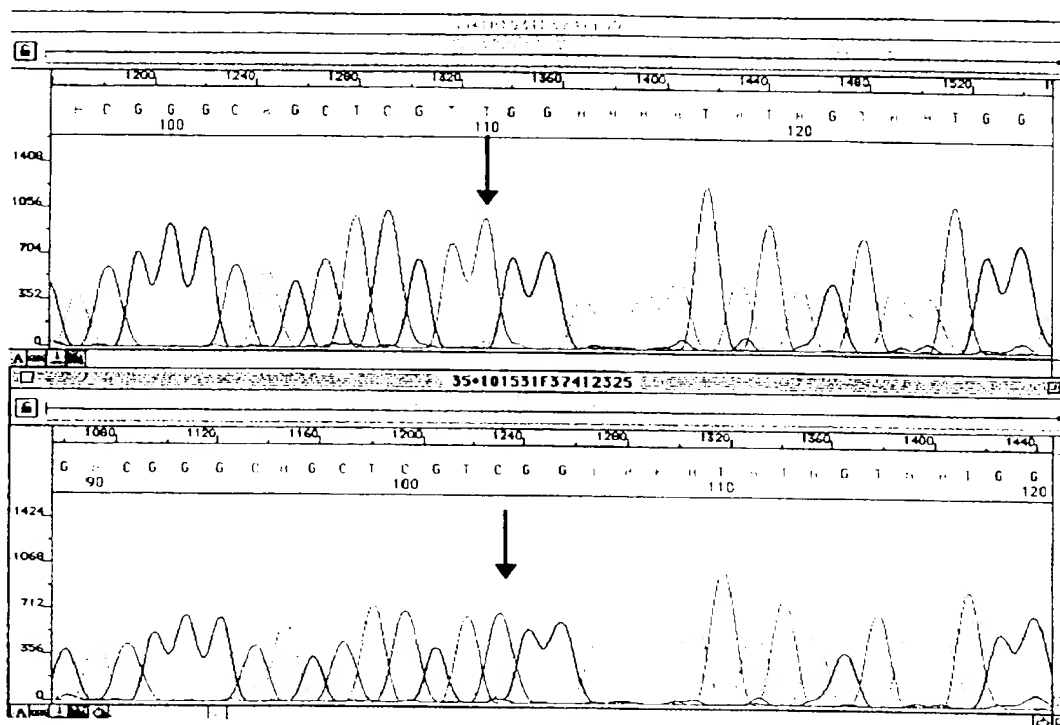|	
Wild Type (human foetal brain)	T/T
Variant Type (human adult brain)	T/C
Polymorphism Position	3554
RFLP	-

FIGURE 6
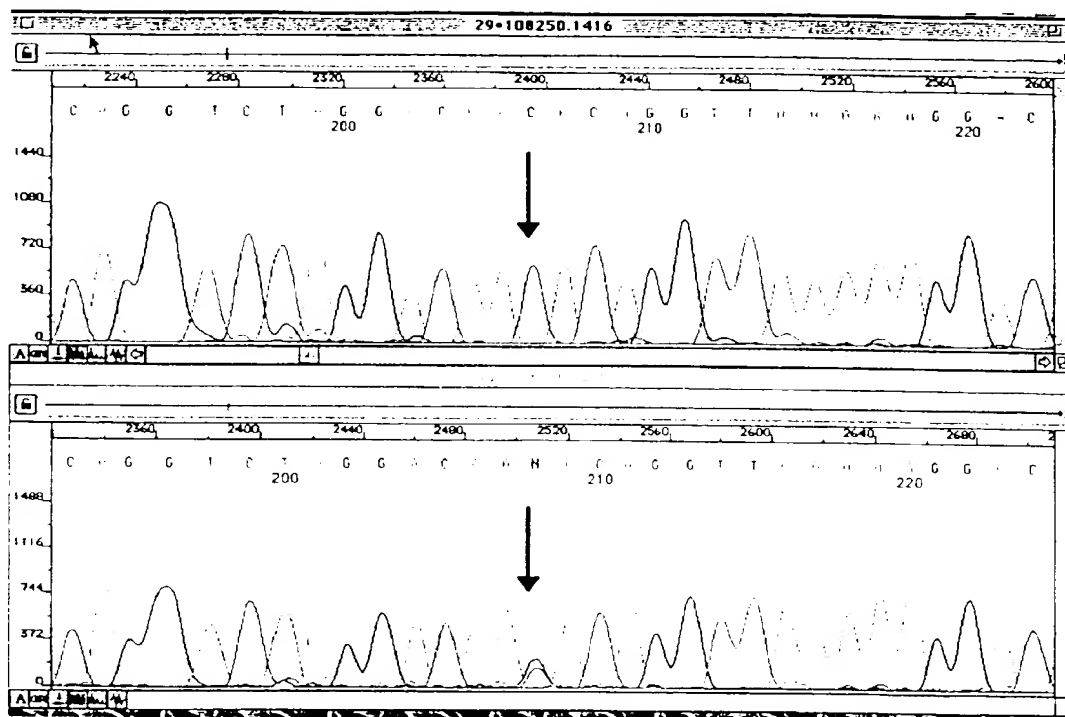
Wild Type (GM1416)	C/C	
Variant (7225)	C/G	
Position	4828	

FIGURE 7

Primer sequences derived from BAC and used on lymphoblastoid cell lines from BPAD Patients.

Homozygous wild type (KK169)   -   T/T

Homozygous variant (KK232)   -   C/C

FIGURE 8

Figure 9

```
TGCTGCAAGTGACAGGTTCCAAGAAGCCCGAGGGCTCAGAGCTGAATGATGAAGCGC
AGTCCCCAAAGTGCCTGGCCACCCCTCCCTCCCTGGATCACTGCTGCCTGGGCTTGA
TTGATTGATTGATTGATTGATTGATTGATTTTGAGAGAGATTCTCACTGTCACCCAG
GCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAGCCTCTGCCTCCCGGGTTCAAG
CAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACGCGCCACCACAC
CCAGCTAATTTTGTATTTTTAGTAAAAGACGGGGTTTCACCATGTTGGGCCAGGATG
GTCTTGATCTCCTGACCTCATGATCCACCCGCCCCGGCTTCCAAAGTGCTGGGATAC
AGGCATGAACCCGACGCGCCCAGCATGGACATTTTTTTTAATCCCCTGCCCTTTTC
TTGNGGCATAATTCATTGCAGGTCTCTTCTATACAGATCATGGAAAACACATTTTCT
TAACTGAGTTNTTATTATTTATACCCAGNCACCTCATGACANNTTTACCCTGTTACA
NACAAAATGGGCACCTGCCAAAANCAACTTTNATATAAGGATGCTCCAGGCCT
```

Tetranucleotide repeat underlined
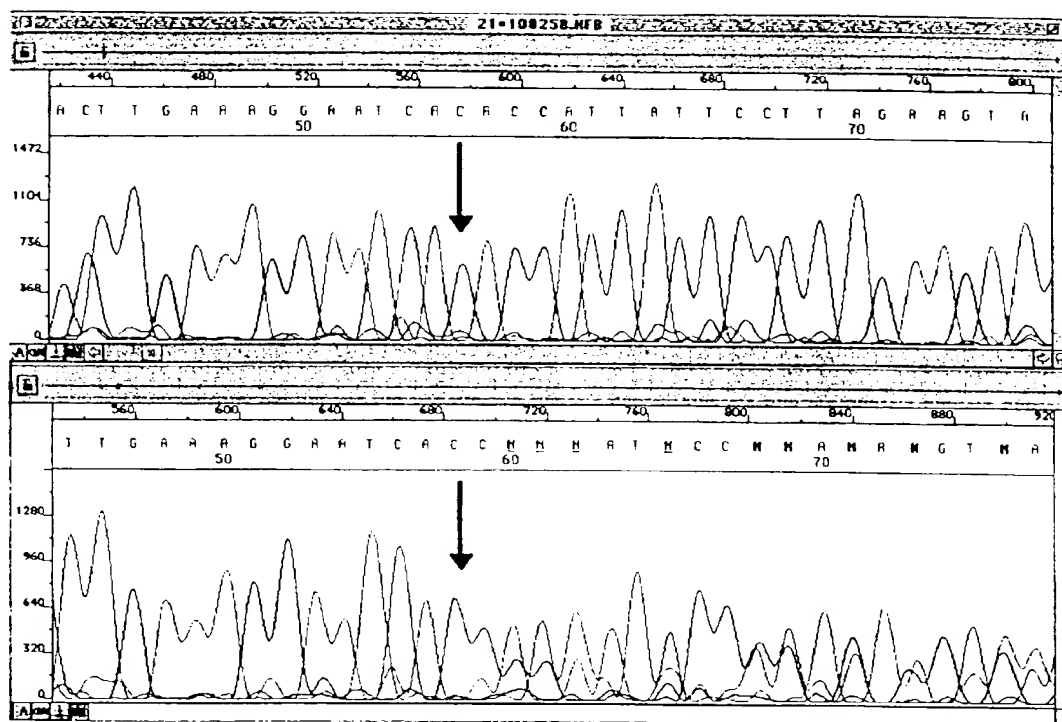
Top electropherogram (human foetal brain) - wild type

Lower electropherogram (7225)   - heterozygous variant

Arrow indicates the position of the C+C insertion - position 4032

FIGURE 10